Transcripts – Speaking of Mol Bio: S1E2

Steve Lewis 00:09
Welcome to *Speaking of Mol Bio*, a new podcast series about molecular biology and its trending applications in life sciences. I'm Steve Lewis.

Dr. Gabriel Alves 00:19
And I am Dr. Gabriel Alves.

Steve Lewis 00:21
In our first season of *Speaking of Mol Bio*, we're focusing our conversations on four exciting application areas: CRISPR cell engineering, multi-omics, exosomes, and single cell analysis, and today we're diving into multi-omics with Dr. Chris Whelan.

Dr. Gabriel Alves 00:38
Chris is the director of neuroscience and data science at Johnson & Johnson and the chair of the UK Biobank Pharma Proteomics Project. He is passionate about using neuroimaging, genetics, and proteomics to better understand neurodegenerative and neuropsychiatric illness. We hope you enjoy our conversation.

Dr. Chris Whelan 01:03
I like to think in terms of bigger picture science, so you know, sometimes people have different definitions of what omics is or multi-omics is, so I like to think of it as the comprehensive assessment of a set of molecules, you know, along that process of the central dogma of biology, right, so, so going from DNA to RNA to protein, and then protein degradation to metabolites. So, when you're attempting to comprehensively characterize the molecules that are involved in in one of those steps, I guess you could call it omics, right? So, you know, proteins, proteomics, you know, genetics, it's genomics. And when you're attempting to characterize multiple steps, it's multi-omics. So, I like how it’s looking at everything from the blueprints of the end product.

Dr. Gabriel Alves 01:47
How is multi-omics helping advance the field? Any field in science?

Dr. Chris Whelan 01:55
Sure, yeah. So, yeah, cancer is a good example. And I feel like as someone who works predominantly in neuroscience that we can learn a lot from oncology. Neuroscience, over the last decade or two has been somewhat rigid in its definitions of most CNS illnesses, something like Alzheimer's disease, I feel that that's more than one disease. And the issue is, well, you know, how do you actually split it up into more than one disease? You can't really do it using the clinical scales. So, you really have to go to the underlying biology. And that's where multi-omics comes in, you know, you look at gene expression, protein levels. Obviously, there's CSF proteomics as well. And, you know, if we start digging into that data, it can really help us subtype the kinds of conditions that we're interested in.

Steve Lewis 02:44
The process that you follow kind of approaches the drug discovery pipeline. And I'm curious, do you start with biomarkers as kind of your initial vision for where you want to go? Do you see something in the data and that inspires you to target something and then maybe design a molecule downstream of that? Or is it a less linear process in your multi-omics approach?

Dr. Chris Whelan 03:14
Yeah, that's a really fun question. And honestly, the answer is it depends on what stage of the drug development process you're working at. And it has applications across the spectrum of drug development. So, if we start at the beginning, right, using multi-omics, particularly genomics, so genetics, that has been positioned as a tool that could potentially increase the success of drug discovery of drug development, there's been some recent studies over the last few years by companies like AbbVie and AstraZeneca. And they've taken a look at their legacy drug development pipelines and look to see of those programs that made it to the clinic and those that didn't, which had supporting evidence from human genetics, and which didn't. And what I mean by that is, you know, supporting evidence like, like a GWAS (genome-wide associated study) association with the disease that they wanted to treat at the protein product of the GWAS hit, and, you know, in, in most cases or twice, you know, twice as likely, those programs are going to have genetic support, that make it to the clinic. So, genomics now is being positioned as a tool that we could use to increase the success of drug discovery. So, that's the start of the development process. But then, to your point about biomarkers. Again, it depends on the use case for biomarkers. If we want to use them as sort of exploratory tools to understand disease biology, then we start applying those at a pretty early stage. So that's, we know about amyloid and tau in Alzheimer's disease, but we know there's lots of other pathways involved in that disease as well. So, why don't we apply multiplex proteomics and transcriptomics to learn more about those different pathways and how they're up and down on Alzheimer's, you know, that might happen at the very beginning or maybe some point during the preclinical development of the drug? And then you get to Phase 1. And again, biomarkers are probably going to be important then in terms of safety monitoring, in terms of target efficacy. So, is your drug actually binding the target? And then as you move forward, you know, even potentially more important for a stratification of the patients, you know, are we getting the right patients for our clinical trials, the case of Alzheimer's disease, you have programs that target tau protein, so there's no blood tests that are being used to actually stratify people who have the right level of tau, and bring those into our trials to increase the chances of success. So, really, it can be applied, multi-omics can be applied at any stage of the drug development process. And it's important on each stage for different reasons.

Dr. Gabriel Alves 05:54
That must be very rewarding, especially working with the diseases that are common and very serious, schizophrenia, you mentioned Alzheimer's. But following these other diseases, similar to bipolar disorder, how is the multi-omics field helping also all these other diseases as you're in the field? I would like to hear how these treatment and research is progressing for those conditions as well.

Dr. Chris Whelan 06:26
There is a certain level of pathology that we can detect already, we can detect the amyloid plaques and tau tangles. But as we're seeing from recent clinical trials, those proteins might not tell the entire story of that disease, there are probably other pathways at play that we might also want to be looking into for the development of new medicines. So, that's where multi-omics comes in. And, you know, moving to other diseases, you know, schizophrenia, bipolar, I mean, I'm personally very passionate about one day, having a blood test where that actually tells you know, whether you have schizophrenia, or what type of schizophrenia you have. It might be a pipe dream, but I feel the only way that we're going to get a better understanding and better diagnosis and treatment of those diseases is to look at every aspect of those diseases using different omics approaches. So, look at gene expression, look at protein levels, metabolite levels, you know, develop polygenic risk scores based on GWAS, bring it all together and just

look at everything holistically and get a sense of whether we can actually subtype these illnesses and find, you know, a little bit. This is a little bit of a cliche at this point. But I really do think that multi-omics is going to help us come closer to precision medicine where we're finding the right drugs for the right patients at the right time.

Steve Lewis 07:53
Gene analysis, I think, is one area, I know, within our company, we have a few different pieces of software, data analysis tools that can help to optimize gene expression, as one example, but I'm curious what, what technology gaps do you see right now, if any, to making that become a reality? Or is it more a workforce and training challenge to be able to tackle that multi-perspective approach?

Dr. Chris Whelan 08:29
It is partially a technology limitation. I mean, these technologies are incredibly exciting, we're not quite at the stage where they're the finished product if that makes sense. You know, in the case of proteomics, again, not to sound like a broken record, but that's a really exciting new field that could help really bring us closer to actual precision medicine. But we're not capturing the entire proteome yet, you know, with mass spec, you know, that's, you know, that's almost like the gold standard, the most of the most widely applied kind of multiplex proteomics, but it's not high throughput. So, there's issues around having, you know, overcoming that and bringing mass spec into the mainstream or being more widely employed on a larger number of samples. And there's companies working on that. Biognosys and Ceres and many others. But in terms of the affinity-based techniques that I mentioned earlier, the aptamer and antibody-based techniques, you know, at the moment, you know, you're going to get up to 7,000 proteins detected using those techniques. And the question is, can we go higher? What is the complete proteome in blood plasma, in blood serum? And does it look different than in CSF or in brain tissue? There's a lot of unanswered questions that you know, a lot of smart people at these different companies are currently interrogating about how can we make these platforms better? How can we increase our coverage and make sure that we're capturing as comprehensive a picture of the proteome as possible.

Dr. Gabriel Alves 08:35
Following up where this field goes, where you think this field is going in the next 10 years?

Dr. Chris Whelan 09:27
I think the most obvious direction is going to go in is even bigger scale. So, again with UK Biobank, we show that you can do omics on a very, very large scale, but we didn't do the entirety of UK Biobank. We did 55,000 people, and there's half a million people in there. So, we're not quite ready to get there yet. But I think in the next three or four years, we will be. Not just for proteomics, you know, some of these other omics technologies as well, single cell transcriptomics has really caught on over the last few years. So, I think that that's going to be even more widely applied than it is now. I think advances in machine learning are going to help us integrate everything a little better. I'm currently that's a big area of focus for me is, you know, how do we actually bring together these different data sources? Whether it's at the microscopic level with neuroimaging or a more sort of microscopic level, you know, with blood proteins? And how do we throw them all into an algorithm that's going to be able to pull out the most important features that are predicting your, your disease or predicting the progression of your disease? So, I think the next probably 4, 5, 6 years, maybe even 10 years are going to be focused around doing that kind of research to figure out, you know, what's the best way of predicting progression for disease X, or just diagnosis of disease Y, and once we've done that groundwork, I mean, what I love to see when I'm in my mid-40s, is walking into a doctor's office,

and actually being able to use these advances these discoveries, to have a diagnostic and have a blood test, or a clinical test that can actually pinpoint the disease you have and the subtype of the disease that you have. So, I think that the first part of my answer, I think, that's, definitely it's happening, and it will continue to happen, and we will move to a much bigger scale. Second part, I don't know that's, that's a dream. I'm not sure it will happen, I'm hoping it will happen. So, fingers crossed, I can, I can be one of many, many, many people who can try to get it to happen.

Steve Lewis 12:22
So, it's almost like a systems-based perspective. And it's interesting, because a lot of times when you talk about the life sciences, you'll have somebody say, oh, I'm a molecular biologist, or oh, I'm a cellular biologist. And it's really interesting, especially when you mix data into the, into the conversation, you're almost blurring the lines, and you almost have to between the disciplines to really study the whole system of what's being looked at. So, I guess that leads me to just ask this, this general question is, for people who are looking to get into the life sciences, who might have that more of an analytical background, or even like statistics, or math, or computer engineering, what one of the common things that you hear for from people in some in Silicon Valley these days is, biology is just a computational problem waiting to be solved. And they say that without context of understanding necessarily how broad life is, right, essentially. So, I'm curious what would be in your mind a way to kind of bridge that gap?

Dr. Chris Whelan 13:43
I would start by not trusting what Silicon Valley will say about biology. If we've learned any lessons from any unnamed diagnostics companies, the whole, you know, fake it till you make it, it doesn't work for biology, doesn't work for medicine. And I think that that's been shown on a very, very high, you know, high profile. So, you need basically, you know, put very simply, you need the biologists, the scientists to be working hand-in-hand with the data scientists and the tech people, right, I think you need to bring those kinds of expertise, expertises together, you know, again, broken record, but going back to the UK Biobank project, that was that was set up as a as a proteomics project by a consortium that was, you know, overwhelmingly geneticists, right. And genetics is not proteomics, they're different fields, they're very different fields. So, while setting that up, and leading that one of my first priorities was, well, you know, we need to get proteomics experts into this consortium too and so I did like, you know, Bradford Gibson, Brad Gibson from Amgen. He came in and he's kind of a world expert on mass spec and proteomics in general. And he's been a really important asset to that consortium. I don't think it would have operated as well as it did without his proteomics expertise. So, just to speak to your point, maybe I'm being a little over overly abstract in my answer, but I think if we had moved forward with that consortium, as a genetics consortium, doing proteomics, I don't think it would have been as successful. We needed to pull in the people with that expertise and work together and learn to speak each other's languages. So, I think on a broader level, you know, you know, in our field, I think the same thing needs to be happening where all of the right people with the right expertise are talking to one another. And you have a couple of people who are helping them, who are helping bring them bring them together who can see the bigger picture.

Steve Lewis 15:49
We hope that you're enjoying this episode of *Speaking of Mol Bio*. We wanted to take a quick moment to tell you about the Invitrogen School of Molecular Biology. It's a great educational hub for molecular biology with rich and reliable technical content, designed for new and experienced molecular biologists alike. Check it out today at thermofisher.com/ismb. And now back to our conversation.

Dr. Gabriel Alves 16:21
I have a couple of questions. One is in regards the results of your huge project, the proteomics project that you did. And the second question, it's totally different. If you could talk a little bit more about neuroimaging, I'm very curious to know what you're looking for.

Dr. Chris Whelan 16:43
So, for the proteomics project, it's funny because it's it, as we alluded to earlier, it's splintered into many different projects. But the one thing that we agreed to do together across the 13 companies was that protein GWAS, right? So, and we run genome wide association studies across the first 1,500 protein measures that we have access to, put that on Bio Archive recently. And Ben Sun from Biogen is the first author on that. Overall finding was that we identified over 10,000 PQTLs (protein quantitative trait loci), snips influencing protein concentrations, and 85% of those were new. So, there's, there's a lot of, you know, biological vignettes that we have in there, we have some new insights into the inflammasome potential new targets for COVID-19 severity. But we were also, you know, I was really impressed with how much the 13 companies wanted to work together on this. But there was a certain point at which we had to stop collaborating, where it got into, you know, target discovery for diseases, that one, you know, that, you know, four or five different companies were interested in. At that point, we had to stop and say, Okay, now we go our separate ways, and we work on our, you know, our IP, that's of highest interest to us. But, basically, the paper that's, that's on Bio Archive, it's, it's laying out the foundation for this project. Here's what we did, here's an initial PGWAS (protein genome-wide association study), and here's some initial insights. And now, you know, these data are going to come online to all approved UK Biobank researchers in March of 2023. And at that point, they can use that paper as a, you know, well currently a manuscript, but hopefully, eventually, a paper as a, as a resource, or as a sort of a touch point for the work that they do downstream. So, you know, I'm we're obviously we're all doing work downstream, we found, you know, new drug targets for Alzheimer's and Parkinson's, there's new biomarkers for some of the drug programs that we have internally based on, you know, one good example is we looked at loss of function effects on the genetic level. So, you take all your protein truncating variants across the genome, that are expected to have a loss of function affecting the protein, and you check to see whether they actually do, and when those PTVs, those protein truncating variants, are in cis, so close to the encoded protein 99% of the time, they are associated with reduced protein, which is consistent with biological loss of function. And the reason that that's important is great, you can take your *in silico* loss of function and look at it at the proteomic level and see that there does indeed seem to be loss of function of that protein, but there's often some trans signals as well for the very same gene variants. So, maybe, you know, loss of function of gene X leads to reduced protein X, but it also seems to change concentrations of protein Y and protein Z. So, they might be new biomarkers. Or they might tell us about when we actually develop a drug that down regulates gene X or protein X, this is what's going to happen. And this is what we might want to measure. So, that's really cool to me. But yeah, that's just one example. There's just so much you can do with these data. And I can't wait until the academic community gets access to it. Because even across 13 pharmas, I don't think we have the hands to do everything we want to do.

Dr. Gabriel Alves 20:20
Chris, the second part of my question was about neuroimaging. So, if you could talk about what you see in your neuroimaging, what are you looking for? And what are some exciting results you can share with us?

Dr. Chris Whelan 20:33

Yeah, no, absolutely. Another big field neuroimaging. And, you know, lots of different kinds of neuroimaging. So, what I specialized in during my PhD was structural neuroimaging. So, looking at gray matter, diffusion, imaging, and looking at white matter organization. Lots of exciting things I'd mentioned earlier that I did my postdoc with the Enigma Consortium, and they they've done a phenomenal job of bringing imaging to very large scale by getting neuroimaging labs from all across the world to process the scans they've already collected in a standardized way. And then, you know, do cross sectional analyses, and then meta- analyze findings together. And the rationale behind that is if you're to completely retrospectively do a meta-analysis on all the existing published neuroimaging studies, it's going to be noisy and messy, because the underlying processing protocols are going to be different across these sites. So, what Paul and the Enigma Consortium was able to show is that when you get labs to agree to process their scans uniformly across, you know, tens, in some cases, hundreds of sites, you get a much cleaner signal, and you get to see some really cool things about the underlying biology of different brain diseases. So, in my case, I led the Enigma Epilepsy Working Group and we found that, you know, there were very robust structural changes, gray matter changes, and in the thalamus, and in the precentral gyrus across a number of different epilepsy subtypes. That wasn't really shown consistently at a level where the P values were very, very low. And everything looked very sort of solid and robust. So, you know, that's one exciting thing, I think the Enigma Consortium is still going very strong, and, you know, allowing us to do neuroimaging at a scale that we hadn't before, because it's expensive, right? So what you saw maybe in the late 90s, and early 2000s, was neuroimaging being done, you know, on maybe, you know, 50 cases and 50 controls, and Enigma has enabled it to be done on you know, in some cases, you know, 5,000 cases, 5,000 controls, and then add to that UK Biobank, because they're not just doing proteomics in UKB, they're doing imaging as well, they just announced that they're going to do repeat imaging of 60,000 people. So, we're going to have, you know, a longitudinal neuroimaging study in 60,000 people, the largest in the world. So, I guess that's speaking to it on a very high level. And what are we actually learning from neuroimaging? You know, quite a lot. I think that diffusion imaging is helping us get a better grip on white matter organization and epilepsy and schizophrenia. You know, again, Enigma Schizophrenia showed that white matter microstructural organization is more widely disrupted than maybe people previously knew in schizophrenia. Functional neuroimaging, which I didn't do during my PhD, but I've collaborated with folks that have expertise in functional neuroimaging, that's going to be critical as well, you know, looking at disturbances the different functional networks in the brain to the bold signals. So, we're looking at these techniques like global brain connectivity and trying to tie that back to genetics and to omics. So, can we identify a signature, you know, when somebody goes into a scanner, and just rests, and you have people that might have a certain disease like, you know, bipolar disorder, and people that don't have that disease. And then look at their resting state connectivity, look at their global connectivity measures, see whether there are differences and if there are differences, what networks are we seeing those differences in, map those back then to gene expression, potentially, proteomics, genetics, and that might actually get us much closer to developing better psychiatric drugs. So, lots of exciting developments in neuroimaging.

Dr. Gabriel Alves 24:42
What kinds of markers or contrasts that you use for your neuroimaging and are you looking for something else besides structure?

Dr. Chris Whelan 24:52
Yeah, most of the imaging that I did, and have been doing doesn't require markers or tracers. But, obviously, those are, those are very important when it comes to PET imaging. So, for Alzheimer's disease again, going back to AD the amyloid PET tracers and tau PET tracers are very important to diagnosis of those illnesses. So, in order to actually be diagnosed as someone

with Alzheimer's disease, the clinician needs to show evidence of high amyloid accumulation. And you can either do that with a spinal tap, which is obviously a pretty nasty, scary procedure. Or you can put the patient in a scanner, a PET scanner, give them an amyloid PET scan. So that's a really helpful technique. And there are new PET tracers being developed for, you know, other proteins that might be of interest, CSFRI to try to see whether we can get some inflammatory components in the brain. So, yeah, PET imaging, not something that I've personally analyzed, but super, super important for diagnostics for neurodegenerative illnesses.

Steve Lewis 26:03
I'm curious, what areas for molecular biology could you see being implemented in, let's say, a study that that you just described? Is it really around the characterization or even deeper understanding of sequences or characterization of proteins? I'm just curious, what areas do you see from like that molecular perspective for the future? What's needed? Or do we have all of the tools that are already needed to do that analysis?

Dr. Chris Whelan 26:45
Yeah, I mean, I feel like we never always have the complete set of tools. But I think that we have a pretty good battery to start developing, especially PET tracers, I think, I think going stepping away from imaging and going back to sort of omics and proteomics, I think one, one thing that will be beneficial is to figure out the binding sites of certain antibodies that are being employed in multiplex, like with Olink and figuring out exactly, you know, where the epitopes lie so whether we can do that, figuring out whether I mean, one of the issues with antibodies, and proteomics is that there is an infinite supply. So, I don't know whether that's something we can get around. But it's just a, I guess, an issue that I will raise without necessarily an immediate way to address it. But yeah, those are just some of the things off the top of my head.

Steve Lewis 27:39
And antibodies are getting more and more, I don't want to say complicated, but they're becoming more diverse in how people are thinking about them. I know the FDA just came out with a few new designations for antibody-based treatments, whether it's bispecifics, or even fragment-based treatments. I'm curious for antibodies in particular, do you see that because it's infinite, there's more opportunity in the *in silico* perspective, or like we've seen just a tremendous explosion of antibody treatments over the past five years, is it still something that's absolutely necessary? To kind of identify through brute force analysis in a laboratory?

Dr. Chris Whelan 28:35
I know that this is a kind of a cheap answer because I'm sitting on the fence, but I think that there's room for both. There's room for both, I think that I'm seeing, you know, these, you know, antibody treatments are still going to be important, but we're going to we're pursuing those kinds of treatments in parallel with, you know, as antisense oligonucleotides, ASOs, siRNAs, there's lots of different ways you can make a drug these days, which is fantastic. I really, I'm grateful that I'm coming into drug discovery at the right time, where, when I was doing my PhD, they defined you know, the druggable genome, and it was a certain number of genes that, you know, you could make a drug against, that's, I feel like that's less and less relevant, because there's, you can, you know, depending on the modality, you can, you can drug a lot of the genome now, and so, antibodies are going to still be important, but some of these other techniques will be as well, I think, you know, having antibodies versus the synthetic approaches, maybe stepping away from treatments and going back to actual sort of measurement with antibody-based multiplex and aptamer synthetic, you know, sort of aptamer-based approaches. Again, I think that there's room for both to play. There's been some really interesting papers lately that have looked at antibody-based proteomics, alongside aptamer-based proteomics. And the big

advantage of the aptamer-based is that they're easy to make and you can measure many more aptamers than then you might be able to measure antibodies simultaneously. But what that paper showed, it was from Claudia Langenberg and Maik Pietzner, that there's value in doing both, you get synergistic insights, I think that's actually in the title of the paper: synergistic insights from antibody- and aptamer-based approaches, you know, you might be able to get more proteins and better coverage and, and tighter CVs with the aptamers, but then you might be able to get more specificity with the antibody-based approach. So, in an ideal world, we will be doing both at the proteomic level and in the in the current world, in terms of therapeutics, where, you know, we're definitely using antibodies alongside many other different approaches.

Dr. Gabriel Alves 30:49
As a last question here, what has been an important factor for your success in your career? What are some tips and tricks that you can give for the new folks that are coming into research and academia, especially that we've mentioned a couple times during this interview? What are some tips and tricks you can give to these folks?

Dr. Chris Whelan 31:13
Oh, yeah. Well, I need to think about that. There's, there's so many things I could recommend. I think in terms of what's gone into my success, I think luck is always going to play a role, I wouldn't want to sound too egotistical to say that it was all my hard work and all that kind of stuff. I think that luck is always a certain element and being in the right place at the right time. But in terms of practical tips on, on how to sort of maximize success, find not just prestigious people to work with, or supervisors, PIs, but kind and nice people who are going to pass the ladder down to you. So, I was lucky that I found those kinds of people in my career, you know, Paul Thompson being one of them, and then the people I've worked under in industry have all been, you know, fantastic advocates for me. So, that's one thing. Make sure you're always thinking bigger picture and outside the box. It's important to be an expert in your field. But at a certain point during my postdoc, you know, I saw this meme, and it's, it's difficult to describe, you know, verbally, but, you know, it's better to just show you a picture of it, but it's this big circle. And it's like, here you are, when you do your undergrad, and then your masters or your PhD, and your postdoc, and you know that the outer edge of the circle is this tiny little blip. And this is what you've done. You know, this is what you've contributed to the to human knowledge. So, you know that that was a little bit disheartening. It was funny, I laughed when I saw it, but I also thought, wow, okay, yeah, you know, it's good to be an expert. But at a certain point, I want to take a step back and say how was what I'm doing fitting in to what my peers are doing in other fields. So, always maintaining a line of sight to the bigger picture is definitely a big factor.

Dr. Gabriel Alves 33:01
That was Chris Whelan, director of neuroscience and data science at Johnson & Johnson. If you're interested in hearing even more of today's conversation, you can view the extended video version of this interview by visiting the URL in the episode notes. And if you'd like, consider sharing something you learn on today's episode with a colleague who might also enjoy the show. This episode was produced by Matt Ferris, Sarah Briganti, and Matthew Stock.

Abstract: S1E2

Speaking of Mol Bio **podcast series by Thermo Fisher Scientific**

Episode: S1E2

Guest: Chris Whelan

Thematic topic: Multi-omics

Title: The importance of science in data science

Quotes:

- “I think the next 4, 5, 6, maybe even 10 years are going to be focused around doing the kind of research to figure out what's the best way of diagnosing or predicting progression for disease X, … walking into a doctor's office and actually being able to use these advances, … to have a diagnostic or a clinical test that can actually pinpoint the disease you have and the subtype of the disease that you have.”
- “In the case of proteomics, that's a really exciting new field that could help really bring us closer to actual precision medicine.”

Episode summary:

Join us for this exciting conversation with Chris Whelan of Johnson & Johnson about muli-omics. He does a phenomenal job of explaining the basics and shines a light on some of the challenges of the field, all while conveying the hope of what this could all mean in terms of understanding and treating disease.

Episode notes:

In this episode, we talk with Chris Whelan about the data behind the science of disease research. Chris is the director of neuroscience and data science at Johnson & Johnson, as well as the chair of the UK Biobank Pharma Proteomics Project. He connects the dots between genomics and proteomics and clarifies how omics can be used to understand disease biology to inform drug development for the treatment of disease. The conversation touches on the challenges of defining and collecting a comprehensive biomarker panel, explores the role of data science in disease research, and underscores the importance of involving people who understand biology in applications of data science that can affect human health.

If you enjoy this conversation with a leader in his field, we hope you’ll subscribe to the series to get future episodes as they drop.

Visit https://thermofisher.com/molbioschool to access molecular biology resources and educational content.

Keywords: Precision medicine, molecular biology, proteomics, multi-omics, neuroimaging, data, data science, biology, GWAS, proteins, biomarkers, neuroimaging,